OIPE

#2

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/972,268

DATE: 10/19/2001
TIME: 12:04:43

Input Set : A:\3101-A SEQ Listing.txt
Output Set: N:\CRF3\10192001\I972268.raw

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 3 <110> APPLICANT: Baum, Peter R.
 4         Fanslow, William C.
 5         Lofton, Timothy E.
 6         Sorensen, Eric A.
 7         Youakim, Adel
 9 <120> TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND
USE THEREOF
11 <130> FILE REFERENCE: 3101-A
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/972,268
14 <141> CURRENT FILING DATE: 2001-10-05
16 <150> PRIOR APPLICATION NUMBER: 60/238,557
17 <151> PRIOR FILING DATE: 2000-10-05
19 <160> NUMBER OF SEQ ID NOS: 39
21 <170> SOFTWARE: PatentIn version 3.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 3147
25 <212> TYPE: DNA
26 <213> ORGANISM: homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (1)..(1626)
31 <223> OTHER INFORMATION:
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37 1               5                  10                  15
39 ctc ctc gga gcc ggg ctc ctg ctg cag ccc ccg acg cca cct ccg ctg        96
40 Leu Leu Gly Ala Gly Leu Leu Leu Gln Pro Pro Thr Pro Pro Pro Leu
41             20                  25                  30
43 ctg ctg ctg ctc ttc ccg ctg ctg ctc ttc tcc agg ctc tgt ggt gcc       144
44 Leu Leu Leu Leu Phe Pro Leu Leu Leu Phe Ser Arg Leu Cys Gly Ala
45         35                  40                  45
47 tta gct gga cca att att gtg gag cca cat gtc aca gca gta tgg gga       192
48 Leu Ala Gly Pro Ile Ile Val Glu Pro His Val Thr Ala Val Trp Gly
49     50                  55                  60
51 aag aat gtt tca tta aag tgt tta att gaa gta aat gaa acc ata aca       240
52 Lys Asn Val Ser Leu Lys Cys Leu Ile Glu Val Asn Glu Thr Ile Thr
53 65                  70                  75                  80
55 cag att tca tgg gag aag ata cat ggc aaa agt tca cag act gtt gca       288
56 Gln Ile Ser Trp Glu Lys Ile His Gly Lys Ser Ser Gln Thr Val Ala
57                 85                  90                  95
59 gtt cac cat ccc caa tat gga ttc tct gtt caa gga gaa tat cag gga    ,  336
60 Val His His Pro Gln Tyr Gly Phe Ser Val Gln Gly Glu Tyr Gln Gly
61             100                 105                 110
63 aga gtc ttg ttt aaa aat tac tca ctt aat gat gca aca att act ctg       384
64 Arg Val Leu Phe Lys Asn Tyr Ser Leu Asn Asp Ala Thr Ile Thr Leu
65         115                 120                 125
67 cat aac ata gga ttc tct gat tct gga aaa tac atc tgc aaa gct gtt       432
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ENTERED

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68 His Asn Ile Gly Phe Ser Asp Ser Gly Lys Tyr Ile Cys Lys Ala Val
69     130                 135                 140
71 aca ttc ccg ctt gga aat gcc cag tcc tct aca act gta act gtg tta      480
72 Thr Phe Pro Leu Gly Asn Ala Gln Ser Ser Thr Thr Val Thr Val Leu
73 145                 150                 155                 160
75 gtt gaa ccc act gtg agc ctg ata aaa ggg cca gat tct tta att gat      528
76 Val Glu Pro Thr Val Ser Leu Ile Lys Gly Pro Asp Ser Leu Ile Asp
77                 165                 170                 175
79 gga gga aat gaa aca gta gca gcc att tgc atc gca gcc act gga.aaa      576
80 Gly Gly Asn Glu Thr Val Ala Ala Ile Cys Ile Ala Ala Thr Gly Lys
81                 180                 185                 190
83 ccc gtt gca cat att gac tgg gaa ggt gat ctt ggt gaa atg gaa tcc      624
84 Pro Val Ala His Ile Asp Trp Glu Gly Asp Leu Gly Glu Met Glu Ser
85                 195                 200                 205
87 act aca act tct ttt cca aat gaa acg gca acg att atc agc cag tac      672
88 Thr Thr Thr Ser Phe Pro Asn Glu Thr Ala Thr Ile Ile Ser Gln Tyr
89     210                 215                 220
91 aag cta ttt cca acc aga ttt gct aga gga agg cga att act tgt gtt      720
92 Lys Leu Phe Pro Thr Arg Phe Ala Arg Gly Arg Arg Ile Thr Cys Val
93 225                 230                 235                 240
95 gta aaa cat cca gcc ttg gaa aag gac atc cga tac tct ttc ata tta      768
96 Val Lys His Pro Ala Leu Glu Lys Asp Ile Arg Tyr Ser Phe Ile Leu
97                 245                 250                 255
99 gac ata cag tat gct cct gaa gtt tcg gta aca gga tat gat gga aat      816
100 Asp Ile Gln Tyr Ala Pro Glu Val Ser Val Thr Gly Tyr Asp Gly Asn
101                 260                 265                 270
103 tgg ttt gta gga aga aaa ggt gtt aat ctc aaa tgt aat gct gat gca     864
104 Trp Phe Val Gly Arg Lys Gly Val Asn Leu Lys Cys Asn Ala Asp Ala
105                 275                 280                 285
107 aat cca cca ccc ttc aaa tct gtg tgg agc agg ttg gat gga caa tgg     912
108 Asn Pro Pro Pro Phe Lys Ser Val Trp Ser Arg Leu Asp Gly Gln Trp
109     290                 295                 300
111 cct gat ggt tta ttg gct tca gac aat act ctt cat ttt gtc cat cca     960
112 Pro Asp Gly Leu Leu Ala Ser Asp Asn Thr Leu His Phe Val His Pro
113 305                 310                 315                 320
115 ttg act ttc aat tat tct ggt gtt tat atc tgt aaa gtg acc aat tcc    1008
116 Leu Thr Phe Asn Tyr Ser Gly Val Tyr Ile Cys Lys Val Thr Asn Ser
117                 325                 330                 335
119 ctt ggt caa aga agt gac caa aaa gtc atc tac att tca gat cct cct    1056
120 Leu Gly Gln Arg Ser Asp Gln Lys Val Ile Tyr Ile Ser Asp Pro Pro
121                 340                 345                 350
123 act act acc acc ctt cag cct aca att cag tgg cat ccc tca act gct    1104
124 Thr Thr Thr Thr Leu Gln Pro Thr Ile Gln Trp His Pro Ser Thr Ala
125                 355                 360                 365
127 gac atc gag gat cta gca aca gaa cct aaa aaa ttg ccc ttc cca ttg    1152
128 Asp Ile Glu Asp Leu Ala Thr Glu Pro Lys Lys Leu Pro Phe Pro Leu
129     370                 375                 380
131 tca act ttg gca aca att aag gat gac aca att gcc acg atc att gct    1200
132 Ser Thr Leu Ala Thr Ile Lys Asp Asp Thr Ile Ala Thr Ile Ile Ala
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                    Input Set : A:\3101-A SEQ Listing.txt
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133 385                   390                 395                   400
135 agt gta gtg ggt ggg gct ctc ttc ata gta ctt gta agt gtt ttg gct      1248
136 Ser Val Val Gly Gly Ala Leu Phe Ile Val Leu Val Ser Val Leu Ala
137                   405                 410                 415
139 gga ata ttc tgc tat agg aga aga cgg acg ttt cgt gga gac tac ttt      1296
140 Gly Ile Phe Cys Tyr Arg Arg Arg Arg Thr Phe Arg Gly Asp Tyr Phe
141                   420                 425                 430
143 gcc aag aac tac att cca cca tca gat atg caa aaa gaa tca caa ata      1344
144 Ala Lys Asn Tyr Ile Pro Pro Ser Asp Met Gln Lys Glu Ser Gln Ile
145             435                 440                 445
147 gat gtt ctt caa caa gat gag ctt gat tct tac cca gac agt gta aaa      1392
148 Asp Val Leu Gln Gln Asp Glu Leu Asp Ser Tyr Pro Asp Ser Val Lys
149     450                 455                 460
151 aaa gaa aac aaa aat cca gtg aac aat cta ata cgt aaa gac tat tta      1440
152 Lys Glu Asn Lys Asn Pro Val Asn Asn Leu Ile Arg Lys Asp Tyr Leu
153 465                   470                 475                 480
155 gaa gag cct gaa aaa act cag tgg aac aat gta gaa aat ctc aat agg      1488
156 Glu Glu Pro Glu Lys Thr Gln Trp Asn Asn Val Glu Asn Leu Asn Arg
157                   485                 490                 495
159 ttt gaa aga cca atg gat tat tat gaa gat cta aaa atg gga atg aag      1536
160 Phe Glu Arg Pro Met Asp Tyr Tyr Glu Asp Leu Lys Met Gly Met Lys
161                   500                 505                 510
163 ttt gtc agt gat gaa cat tat gat gaa aac gaa gat gac tta gtt tca      1584
164 Phe Val Ser Asp Glu His Tyr Asp Glu Asn Glu Asp Asp Leu Val Ser
165             515                 520                 525
167 cat gta gat ggt tcc gta att tcc agg agg gag tgg tat gtt            1626
168 His Val Asp Gly Ser Val Ile Ser Arg Arg Glu Trp Tyr Val
169     530                 535                 540
171 tagcaaccac tgaatgtgac ttaactatgt acaatgttca ttcacactag ttgatcattt    1686
173 tcagattgtt catacttttt cttgaggaag aataagcttt ttcaagttga ttttcaagct    1746
175 tactttttat attctaatct gacaaatgaa aatgtaaaat ctgagttcag tgtatctaag    1806
177 ctgctttaca atttttttttc aatgctgtac tactgtctca agatttaaat tttaatgcag    1866
179 agtactttat tggtgtgagg cacacaggta agaagaaatg tcaacattaa atgtatgact    1926
181 tacttggtac aaaaattttt taaaaaggga actaccttga cattgtgtat taaatgttta    1986
183 cctaagacta taatctcaag tatgatgttt gtttaacata tacctctcaa aatttatcac    2046
185 cactcaatga cactgcatca aaattgacta taaaactaat tcaagaaata tttatatata    2106
187 tttttttaata tacaaaaaat atttagcctg atggaatggc tttcctttc aaacattatt     2166
189 ttctaagttt ctatacaaat gaaatcttta cctctgcata ttaatgagcc ttgccataat    2226
191 tactgtagag tggctttca aagatatttt gttgcactaa aactgtggta gtaaactcag     2286
193 tgaacatgat gtgtggaaga gcataattag ctggtcaata tttttgtcca aaatacctgc    2346
195 aagagtaata aaatacatac ctttcaaaca tgataattat tagtttttttt tttcctttct    2406
197 ggaacatgga ttttggtaca ttagcagtag ccttatttta atgctttatg tcctaaacat    2466
199 actaatagaa atgaaaagac gcagagagag catttcggaa tactgaagta ctagtttta g    2526
201 aaatgagact ttcagccaac aatctataga aagaattta tggaccatct tgttttagtt     2586
203 atttaatgtt gatgttgttc aaatgggtaa atgtacagaa agaaaattt agagtaaact      2646
205 tggaactttg gatataacta gaaaaaacta gattatagaa ttagtcggta acacttgcta    2706
207 atggacattg gcattcatct ccttttcct cctaagtgta tgtatgtgtt ttaagatttc      2766
209 tgtttttacg attaaaactg gaaacatgag gttttttgtt tttgttttttt tacataatta   2826
211 catatattcc ttctgaatca tttatctttt gagaaagaaa tgttacctaa acttcaaatg    2886
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213 tgcttttgt ttgtgaggta attaaattgc ttctacagtg gaggcttaca aaattattgt   2946
215 gacaactatt ttgaagctga aaggatagtt tttctattgc taagtcattt gaaaaagtga   3006
217 ccattttgcc agtgaaatga agtggaagtt agtaggagaa tcataaatta aatatattat   3066
219 tttgttaata aaaaggcaaa gtagtaggta cttttaaac cctcccaacc agccctttct    3126
221 caatattcat caaatctaaa a                                            3147
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236             20                  25                  30
239 Leu Leu Leu Leu Phe Pro Leu Leu Leu Phe Ser Arg Leu Cys Gly Ala
240         35                  40                  45
243 Leu Ala Gly Pro Ile Ile Val Glu Pro His Val Thr Ala Val Trp Gly
244     50                  55                  60
247 Lys Asn Val Ser Leu Lys Cys Leu Ile Glu Val Asn Glu Thr Ile Thr
248 65                  70                  75                  80
251 Gln Ile Ser Trp Glu Lys Ile His Gly Lys Ser Ser Gln Thr Val Ala
252             85                  90                  95
255 Val His His Pro Gln Tyr Gly Phe Ser Val Gln Gly Glu Tyr Gln Gly
256             100                 105                 110
259 Arg Val Leu Phe Lys Asn Tyr Ser Leu Asn Asp Ala Thr Ile Thr Leu
260         115                 120                 125
263 His Asn Ile Gly Phe Ser Asp Ser Gly Lys Tyr Ile Cys Lys Ala Val
264     130                 135                 140
267 Thr Phe Pro Leu Gly Asn Ala Gln Ser Ser Thr Thr Val Thr Val Leu
268 145                 150                 155                 160
271 Val Glu Pro Thr Val Ser Leu Ile Lys Gly Pro Asp Ser Leu Ile Asp
272             165                 170                 175
275 Gly Gly Asn Glu Thr Val Ala Ala Ile Cys Ile Ala Ala Thr Gly Lys
276             180                 185                 190
279 Pro Val Ala His Ile Asp Trp Glu Gly Asp Leu Gly Glu Met Glu Ser
280         195                 200                 205
283 Thr Thr Thr Ser Phe Pro Asn Glu Thr Ala Thr Ile Ile Ser Gln Tyr
284     210                 215                 220
287 Lys Leu Phe Pro Thr Arg Phe Ala Arg Gly Arg Arg Ile Thr Cys Val
288 225                 230                 235                 240
291 Val Lys His Pro Ala Leu Glu Lys Asp Ile Arg Tyr Ser Phe Ile Leu
292             245                 250                 255
295 Asp Ile Gln Tyr Ala Pro Glu Val Ser Val Thr Gly Tyr Asp Gly Asn
296             260                 265                 270
299 Trp Phe Val Gly Arg Lys Gly Val Asn Leu Lys Cys Asn Ala Asp Ala
300         275                 280                 285
303 Asn Pro Pro Pro Phe Lys Ser Val Trp Ser Arg Leu Asp Gly Gln Trp
304         290                 295                 300
307 Pro Asp Gly Leu Leu Ala Ser Asp Asn Thr Leu His Phe Val His Pro
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308 305                   310                315                320
311 Leu Thr Phe Asn Tyr Ser Gly Val Tyr Ile Cys Lys Val Thr Asn Ser
312                   325                330                335
315 Leu Gly Gln Arg Ser Asp Gln Lys Val Ile Tyr Ile Ser Asp Pro Pro
316             340                345                350
319 Thr Thr Thr Thr Leu Gln Pro Thr Ile Gln Trp His Pro Ser Thr Ala
320         355                360                365
323 Asp Ile Glu Asp Leu Ala Thr Glu Pro Lys Lys Leu Pro Phe Pro Leu
324     370                375                380
327 Ser Thr Leu Ala Thr Ile Lys Asp Asp Thr Ile Ala Thr Ile Ile Ala
328 385                390                395                400
331 Ser Val Val Gly Gly Ala Leu Phe Ile Val Leu Val Ser Val Leu Ala
332             405                410                415
335 Gly Ile Phe Cys Tyr Arg Arg Arg Arg Thr Phe Arg Gly Asp Tyr Phe
336             420                425                430
339 Ala Lys Asn Tyr Ile Pro Pro Ser Asp Met Gln Lys Glu Ser Gln Ile
340         435                440                445
343 Asp Val Leu Gln Gln Asp Glu Leu Asp Ser Tyr Pro Asp Ser Val Lys
344     450                455                460
347 Lys Glu Asn Lys Asn Pro Val Asn Asn Leu Ile Arg Lys Asp Tyr Leu
348 465                470        ·        475                480
351 Glu Glu Pro Glu Lys Thr Gln Trp Asn Asn Val Glu Asn Leu Asn Arg
352             485                490                495     ·
355 Phe Glu Arg Pro Met Asp Tyr Tyr Glu Asp Leu Lys Met Gly Met Lys
356         500                505                510
359 Phe Val Ser Asp Glu His Tyr Asp Glu Asn Glu Asp Asp Leu Val Ser
360         515                520        ·        525
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364     530                535                540
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368 <211> LENGTH: 1650
369 <212> TYPE: DNA
370 <213> ORGANISM: Artificial Sequence
372 <220> FEATURE:
373 <223> OTHER INFORMATION: nucleotides 1-21 are from Mus musculus Nectin-3, the rest
are fro
374       m human Nectin-3 alpha
376 <220> FEATURE:
377 <221> NAME/KEY: CDS
378 <222> LOCATION: (1)..(1650)
379 <223> OTHER INFORMATION:
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385 1               5                10                15
387 gca caa ctt tcc tcc gct tct ctc ctc gga gcc ggg ctc ctg ctg cag      96
388 Ala Gln Leu Ser Ser Ala Ser Leu Leu Gly Ala Gly Leu Leu Leu Gln
389             20                25                30
391 ccc ccg acg cca cct ccg ctg ctg ctg ctg ctc ttc ccg ctg ctg ctc     144
392 Pro Pro Thr Pro Pro Pro Leu Leu Leu Leu Leu Phe Pro Leu Leu Leu
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VERIFICATION SUMMARY DATE: 10/19/2001
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Input Set : A:\3101-A SEQ Listing.txt
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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number